

SEQUENCE LISTING

<110> GOLDBERG, EDWARD B.

<120> GENE AND PROTEIN SEQUENCES OF PHAGE T4 GENE 35

<130> 8471-007-228

<140> PCT/US99/13024

<141> 1999-06-11

<160> 8

<170> PatentIn Ver. 2.0

<210> 1

<211> 1119

<212> DNA

<213> Bacteriophage T4

<400> 1

```

atggaaaaat ttatggccga gtttggacaa ggatatgtcc aaacgccatt tttatcgaa 60
agtaattcag taagatataa aataagtata gcgggttctt gcccgttcc tacagcagga 120
ccatcatatg ttaaatttca ggataatcct gtaggaagtc aaacatttag cgcaggcctc 180
catttaagag ttttgaccc ttccaccggg gcatttagtt atagtaagtc atatgcctt 240
tcgacttcaa atgatactac atcagctgtc ttgttagtt tcatgaattc ttgacgaaat 300
aatcgaattt ttgctatatt aactagtggg aagggttaatt ttccctctga agtagtatct 360
tggtaagaa ccgcccggaaac gtctgcctt ccatctgatt ctatattgtc aagatttgac 420
gtatcatatg ctgctttttt tactttttt aaaaagagcta tcgcattttaga gcatgttaaa 480
ctgagtaata gaaaaaggcac agatgattat caaaacttatt tagatgttgtt atttgacagt 540
ttagaagatg taggggctac cggggttccca agaggaacgt atgaaagtgt tgagcaattc 600
atgtcggcag ttgggtggaaac taatgacgaa attgcgagat tgccaaacttc agctgctata 660
agtaaattat ctgattataa tttaatttctt ggagatgttc ttatctttaa agctcagttt 720
tatgtgtatg ctgatttttact tgctcttggg actacaatata tatctatccg tttttataat 780
gcatctaacc gatattttc ttcaacaccaa gctgaattta ctggcaagg tgggtcatgg 840
gaattaaagg agattatgt agttgttccca gaaaacgcag taggattttac gatatacgc 900
cagagaactg cacaagctgg ccaaggtggc atgagaaaatt taagctttc tgaagtatca 960
agaaatggcg gcatttcgaa acctgctgaa ttggcgtca atggtattcg tggtaattat 1020
atctgcgaat ccgcttcacc cccggatata atggtacttc ctacgcaagc atcgtctaaa 1080
actggtaaaat tggttggca agaattttaga gaagtttaa 1119

```

<210> 2

<211> 372

<212> PRT

<213> Bacteriophage T4

<400> 2

Met	Glu	Lys	Phe	Met	Ala	Glu	Phe	Gly	Gln	Gly	Tyr	Val	Gln	Thr	Pro
1				5				10					15		

Phe	Leu	Ser	Glu	Ser	Asn	Ser	Val	Arg	Tyr	Lys	Ile	Ser	Ile	Ala	Gly
								20				25			30

Ser	Cys	Pro	Leu	Ser	Thr	Ala	Gly	Pro	Ser	Tyr	Val	Lys	Phe	Gln	Asp
								35				40			45

Asn	Pro	Val	Gly	Ser	Gln	Thr	Phe	Ser	Ala	Gly	Leu	His	Leu	Arg	Val
								50			55			60	

Phe	Asp	Pro	Ser	Thr	Gly	Ala	Leu	Val	Asp	Ser	Lys	Ser	Tyr	Ala	Phe
								65			70		75		80

Ser	Thr	Ser	Asn	Asp	Thr	Thr	Ser	Ala	Ala	Phe	Val	Ser	Phe	Met	Asn
								85			90			95	

Ser Leu Thr Asn Asn Arg Ile Val Ala Ile Leu Thr Ser Gly Lys Val
 100 105 110
 Asn Phe Pro Pro Glu Val Val Ser Trp Leu Arg Thr Ala Gly Thr Ser
 115 120 125
 Ala Phe Pro Ser Asp Ser Ile Leu Ser Arg Phe Asp Val Ser Tyr Ala
 130 135 140
 Ala Phe Tyr Thr Ser Ser Lys Arg Ala Ile Ala Leu Glu His Val Lys
 145 150 155 160
 Leu Ser Asn Arg Lys Ser Thr Asp Asp Tyr Gln Thr Ile Leu Asp Val
 165 170 175
 Val Phe Asp Ser Leu Glu Asp Val Gly Ala Thr Gly Phe Pro Arg Gly
 180 185 190
 Thr Tyr Glu Ser Val Glu Gln Phe Met Ser Ala Val Gly Gly Thr Asn
 195 200 205
 Asp Glu Ile Ala Arg Leu Pro Thr Ser Ala Ala Ile Ser Lys Leu Ser
 210 215 220
 Asp Tyr Asn Leu Ile Pro Gly Asp Val Leu Tyr Leu Lys Ala Gln Leu
 225 230 235 240
 Tyr Ala Asp Ala Asp Leu Leu Ala Leu Gly Thr Thr Asn Ile Ser Ile
 245 250 255
 Arg Phe Tyr Asn Ala Ser Asn Gly Tyr Ile Ser Ser Thr Gln Ala Glu
 260 265 270
 Phe Thr Gly Gln Ala Gly Ser Trp Glu Leu Lys Glu Asp Tyr Val Val
 275 280 285
 Val Pro Glu Asn Ala Val Gly Phe Thr Ile Tyr Ala Gln Arg Thr Ala
 290 295 300
 Gln Ala Gly Gln Gly Met Arg Asn Leu Ser Phe Ser Glu Val Ser
 305 310 315 320
 Arg Asn Gly Gly Ile Ser Lys Pro Ala Glu Phe Gly Val Asn Gly Ile
 325 330 335
 Arg Val Asn Tyr Ile Cys Glu Ser Ala Ser Pro Pro Asp Ile Met Val
 340 345 350
 Leu Pro Thr Gln Ala Ser Ser Lys Thr Gly Lys Val Phe Gly Gln Glu
 355 360 365
 Phe Arg Glu Val
 370

<210> 3
 <211> 8855
 <212> DNA
 <213> Bacteriophage T4

<400> 3
 taggagcccg ggagaatggc cgagattaaa agagaattca gagcagaaga tggctggac 60
 gcagggtggtg ataaaaataat caacgtagct ttagctgatc gtaccgtagg aactgacggt 120
 gttaacgttg attacttaat tcaagaaaaac acagttcaac agtatgatcc aactcgtgga 180
 tatttaaaag attttgtaat catttatgtat aaccgctttt gggctgctat aatgtatatt 240

caaaaaccag	caggagctt	taatagcgg	cgctggagag	cattacgtac	cgatgctaac	300
tggattacgg	tttcatctgg	ttcataatcaa	ttaaaatctg	gtgaagcaat	tfcggttaac	360
accgcagctg	gaatgacat	cacgttact	ttaccatctt	ctccaatttg	tggtgatact	420
atcgttctcc	aagatattgg	aggaaaacct	ggaggttacc	aagttttat	tgtagctcca	480
gtacaagaatg	ttgtaaacct	tagaggtgaa	caggtagctt	cagtaactat	gactcatcca	540
aagtccacgc	taggtttat	ttttagttaat	cgtctgtggc	aatatgtatgt	tgctgttatt	600
agtagagaaag	ctatagttgt	aacaccagcg	aataacttac	aagcgaatc	caacgatttt	660
atcgtaacgt	gatttacttc	tgctgcacca	attaatgtca	aacttccaag	atttcttaat	720
catggcgata	ttattaattt	cgtcgattta	gataaaactaa	atccgcttta	tcatacattt	780
gttactacat	acgatgaaac	gacttcagta	caagaagftg	gaactcatc	cattgaaggc	840
cgtacatcg	ttgacggtt	cttgcgtt	gatgataatg	agaaaattatg	gagactgttt	900
gacggggata	gtaaagccg	tttacgtatc	ataacgacta	attcaacat	tgcgttcaat	960
gaagaagtt	ttgttattgg	tgcaataac	ggaacaactc	aaacaatttg	gcttaagctt	1020
ccaactaata	tttctgttgg	tgatactgtt	aaaatttcca	tgaattacat	gagaaaagga	1080
caaacagtt	aaatcaaagc	tgctgtatgg	gataaaatttg	cttcttcagt	tcaattgctg	1140
caattccaa	aacgctcaga	atatccacct	gaagctgaat	gggttacagt	tcaagaatta	1200
gttttaacg	atgaaaactaa	ttatgttcca	grrttggagc	ttgcttacat	agaagattct	1260
gatggaaaat	atgggttgt	acagcaaaac	gttccaactg	tagaaagagt	agattcttt	1320
aatgatttca	ctagcagaag	attaggcgta	attgttttag	ctacacaacg	tcaagcttaat	1380
gtcgatttag	aaaattctcc	acaaaaagaa	tttagcaatta	ctccagaaac	gttagctaat	1440
cgtactgcta	cagaaaactcg	cagaggtatt	gcaagaatag	caactactgc	tcaagtgaat	1500
cagaacacca	cattctcttt	tgctgtatgt	attatcatca	ctccctaaaa	gctgaatgaa	1560
agaactgcta	cagaaaactcg	tagaggtgtc	gcagaaaattg	ctacgcagca	agaaactaat	1620
gcggaaccg	atgatatactac	aatcatcact	cctaaaaagc	ttcaagctcg	tcaagttct	1680
gaatcattat	ctgttattgt	aaccttgtt	tctactgcag	gtgctactcc	agcttcttagc	1740
cgtgaattaa	atgtacgaa	tttttataat	aaaacaaactg	ataattttatg	tttttcacat	1800
aaagctttgg	atcagtataa	agctactcca	acacagcaag	gtgcagtaat	tttagcagtt	1860
gaaagtgaag	taattgtctgg	acaaagtctag	caaggatggg	caaattgtgt	tgtaacgcca	1920
gaaacgttac	ataaaaaagac	atcaactgtat	ggaagaatttg	gtttaatttg	aattgctacg	1980
caaagtgaag	ttaatcagg	aactgtttat	aactgtttat	tcactcccaa	aactttaat	2040
gaccgttag	caactgaaag	ttttttttgt	actctgtcag	ttgctacaca	agttgaattc	2100
gacgcaggcg	tcgacgatac	tcgtatctt	acaccattaa	aaattttaaaac	cataggatata	2160
agtactgatc	gtacttctgt	tgttgcctca	tctggattag	ttgaatcagg	aactctctgg	2220
gaccattata	cacttaatat	tcttgaagca	aatgagacac	aacgtggtac	acttcgtgt	2280
gctacgcagg	tcgaagctgc	tgcggaaca	ttagataatg	ttttataaaac	tcctaaaaag	2340
cttttagtta	ctaaatctac	tgaagccaa	gaggggttta	ttttttttgtc	aactctgtct	2400
gaaactgtga	ctgaaacgtc	agcaaatact	gtctatctc	caaaaaattt	aaatggatt	2460
gfcgagatgt	aacctacttg	ggcgactct	actgcataaa	gagggtttgt	aaaatttca	2520
tctggttcaa	ttacattcgt	tgtttaatgt	acagtccgtt	ctacccaaaga	tttagaactg	2580
tatgagaaaa	atagctatgc	ggtatcccca	tatgaattaa	accgtgtatt	agcaatttat	2640
ttgcccactaa	aagcaaaagc	tgctgataca	aattttattgg	atggtctaga	ttcatctcag	2700
ttcattctgt	gggatattgc	acagacggtt	aatgtttcac	taaccttaac	ccaaacaaacg	2760
aatctgtat	ccccctttgt	atcatctgt	actgtgtaat	ttgggtgttc	attggccgt	2820
aatagaacat	ttaccatctcg	ttataatcg	gccccgacta	gtatcgttt	cgaaaaaggt	2880
cctgcatccg	gggcaaatcc	tgcacagtca	atagatattc	gtgtatgggg	taaccaattt	2940
ggcggcggta	gtgatacgc	ccgttcgaca	gtgtttgaag	ttggcgtatga	cacatctcat	3000
cacttttt	ctcaacgtaa	taaagacggt	aatatagcgt	ttaacattaa	tggtactgt	3060
atgccaataaa	acattaatgc	tcccggttt	atgaatgtga	atggcactgc	aacattcggt	3120
cgttcagtt	cagccaatgg	tgaatttcatc	agcaagctcg	caaattgttt	tagacaata	3180
aacgggtatt	acggattttt	tattctgtat	gtgccttca	ataccttattt	tttgtctact	3240
gcagccgggt	atcagacttg	ttgttttaat	ggattacgcc	cattttat	taataatcaa	3300
tccggtcaga	ttacaatttg	tgaaggctta	atcattgcca	aagggtttac	tataaaattca	3360
ggcggtttaa	ctgttaactc	gagaattcgt	tctcagggtt	ctaaaacatc	tgattttat	3420
acccgtgcgc	caacatctga	tactgttaga	ttctgttcaa	tcgatattaa	tgatttcagcc	3480
acttataacc	agtccccggg	ttatrtttaa	atgggtgaaa	aaactaatga	agtactgtgg	3540
cttccatct	tagaaacgtgg	cgaagaagtt	aaatctctg	gtacactgac	tcagtttgg	3600
aacacacttg	attcgcttta	ccaaagatttg	attacttac	caacgcgcg	agaagcgcgt	3660
accactcgct	ggacacgtac	atggcagaaa	acccaaaact	tttggtcaag	ttttgttcag	3720
gtatcttgc	gaggttaaccc	tccicaacca	tctgatatcg	gtgccttacc	atctgataat	3780
gctacaatgg	ggaatcttac	tattctgtat	ttctgtcgaa	ttggtaatgt	tcgcattgtt	3840
cctgaccacg	tgaataaaac	ggtttaattt	gaatgggttg	aataagaggt	attatggaaa	3900
aattttatggc	cgagattttgg	acaaggatgt	gtccaaacgc	cattttatcg	gaaagtaat	3960
cagtaagata	taaaaataagt	atagcgggtt	cttgcggcgt	ttctacagca	ygaccatcat	4020
atgttaaatt	tcaggataat	cctgttaggaa	gtcaaacatt	taggcgcagg	ccttcattta	4080
agagtttttg	acccttccac	cggagcatta	gttgatagta	agtcatatgc	tttttcgact	4140

tcaaatgata	ctacatcagc	tgctttgtt	agttttcatg	aatttcttga	cgaataatcg	4200
aattttgtct	atattaacta	gtggaaaggt	taattttcct	cctgaagtag	tatcttgggt	4260
aagaaccgcc	ggaacgtctg	cctttccatc	tgattctata	ttgtcaagat	ttgacgtatc	4320
atatgtctct	tttatactt	cttctaaaag	agctatcgca	ttagagcatg	ttaaactgag	4380
taatagaaaa	agcacagatg	attatcaaac	tattttagat	gttgttattg	acagtttaga	4440
agatgttagg	gctaccgggt	ttccaagaag	aacgtatgaa	agtgttgagc	aattcatgtc	4500
ggcagtgtt	ggaactaata	acgaaatttg	gagattgcca	acttcagctg	ctataagtaa	4560
attatctgt	tataattttaa	ttctggaga	tgttttttat	ctttaagctc	agtttatatgc	4620
ttgtatgtat	ttacttgctc	ttggaaactac	aaatataatct	atccgtttt	ataatgcattc	4680
taacggatat	atttcttcaa	cacaagctga	atttactggg	caagctgggt	catggaaattt	4740
aaaggaagat	tatgttagtg	ttccagaaaa	cgcagtagga	tttacgatat	acgcacagag	4800
aactgcacaa	gctggccaag	gtggcatgag	aaatthaagc	ttttctgtaag	tatcaagaaa	4860
tggcggcatt	tcaaaccctg	ctgaaatttg	cgtcaatgtt	attcgtgtt	attatatctg	4920
cgaatccgt	tcacccctgg	atataatgtt	acttcctacg	caagcatgt	ctaaaactgg	4980
taaagtgtt	gggcaagaat	tttagagaatg	ttaaatttgag	ggacccttcg	ggttcccttt	5040
ttctttataa	atactattca	aataaagggg	catacaatgg	ctgatttaaa	agttagttca	5100
acaactggag	gctctgtcat	ttggcatcaa	ggaaattttc	cattgaatcc	agccggtgac	5160
gatgtactct	ataaattcatt	taaaatataat	tcagaatata	acaaaccaca	agctgtctat	5220
aacgatttcg	tttcttcaaagc	taatgttggt	actttatgcat	caaaggtaac	atthaacgtc	5280
ggcatttcag	tcccatatgc	tccaaacatc	atggccctac	gcccggattt	ttggggtaac	5340
ggtcatgtgt	ctacttttga	taaagcaaat	atcgatattt	tttcatggta	tggcgttagg	5400
ttaaattctgt	catttggttc	aacaggccga	actgttgtaa	ttaatacacg	caatggtgat	5460
attaacacaaa	aagtgttgtt	gtcggcagct	ggtcaagtaa	gaagtggtgc	ggctgctccct	5520
atagcagcga	atgacccattac	tagaaaggac	tatgttgatg	gagcaataaa	tactgtfact	5580
gcaaatgcaa	actcttagggt	gctacggct	gggtacacca	tgacaggtaa	ttaacagcgc	5640
ccaaactttt	tctcgcagaa	tcctgcatct	tcacccctac	attttccacg	atttgaccaa	5700
atcgtaatta	aggattctgt	tcaagatttc	ggcttatttt	aaggaggactt	atggctactt	5760
taaaacaaat	acaattttaa	agaagcaaaa	tcgcaggaac	acgtctctgt	gctttagtat	5820
tagccgaagg	tgaattggct	ataaaacttaa	aagatagaac	aatttttact	aaagatgatt	5880
caggaaatat	catcgatcta	ggttttgcta	aaggccggca	agttgtatgc	aacgttacta	5940
ttaacggact	tttgagattt	aatggcgtt	atgtacaaac	aggtggaaat	actgttaaacg	6000
gaccattgg	ttctactgtat	ggcgtcactg	gaaaaatttt	cagatctaca	cagggttcat	6060
ttttagtcaag	agcaacaaac	gatacttca	atggccattt	atggtttga	aatggccgtat	6120
gcactgaacg	tggcggtata	tatgtctgccc	cttcaactac	aactgtacggt	gaaatacgccc	6180
ttagggtag	acaaggaaca	ggaagcactg	ccaacagtga	attctatttc	cgctctataa	6240
atggaggcga	atttcaggct	aaccgtattt	tagcatcaga	ttcgtttagta	acaaaacgcg	6300
ttgcgttta	taccgttatt	catgtgcca	aaggattttg	acaatatgtat	tctcactctt	6360
tgtttaat	tgtttatctt	ggaaccggtg	aaacaaatgg	tgttaactat	ttcgttaaaat	6420
ttcgcgttaa	gtccgggtgt	acaattttatc	atggaaatttt	taactgtacat	acaggccttag	6480
ctgatgttgt	ttcttgggtgg	tctgggtata	caccagtatt	ttacttatac	ggtatttgcgt	6540
acgatggcag	aatgattttatc	cgtaatagcc	ttgcatttagg	tacatttact	acaaatttcc	6600
cgtctagtgt	ttatggcaac	gtcgggtgtaa	tggcgatata	gtatcttgtt	ctcggcgaca	6660
ctgtacttgg	tttgtcatac	aaaaaaactg	gtgtatttga	tctagttggc	ggtggatatt	6720
ctgttgcctc	tattactctt	gacagtttcc	gtatgtactcg	taaaggatgtt	tttggcgttgc	6780
ctgaggacca	aggcgcacact	tggataatgc	ctggtacaaa	tgctgtctc	ttgtctgttc	6840
aaacacaagc	tgataataac	aatgctggag	acggacaaaac	ccatatcggtt	tacaatgtcg	6900
geggtaaaat	gaaccactat	ttccgtgtta	caggtcagat	gaatatcaat	acccaacaag	6960
gtatggaaaat	taacccgggt	attttgaat	tggtaactgg	ctctaataat	gtacaattttt	7020
acgctgacgg	aacttattttc	tccatttcaac	ctttaaaattt	agataacgcg	atatttttaa	7080
ctaaatctaa	taatactcg	ggtttttaat	ttggagctcc	tagccaagtt	gatggccacaa	7140
ggactatcca	atgaaacggt	ggtaactcg	aaaggacagaa	taaaaactat	gtgatttattt	7200
aagcatgggg	taactcatttt	aatggccactg	gtgatagatc	tcgcggaaacg	gttttccaag	7260
tatcagatag	tcaaggatat	tatttttatg	ctcatcgtaa	agcttcaacc	ggcgcacgaaa	7320
ctattggacg	tattgaagct	caatttgcgt	gggatgtttt	tgcttaaaggt	attatttgcct	7380
acggaaattt	taggttggtt	gggtcaagcg	cttttagccgg	caatgttact	atgtctaaacg	7440
gtttgtttgt	ccaaagggtgt	tcttttattt	ctggacaaagt	taaaaatttgc	ggaacacgaa	7500
acgcactgt	aatttggaaac	gctgtatattt	gtgttttttt	ccgtctgttc	gaaagtaact	7560
tttatattat	tccaaaccat	caaaatgtaa	gagaaagttgg	agacatccatc	agctttttgt	7620
gacctgttag	aataggattt	aacgtatggca	tggttgggtt	aggaagagat	tcttttatagt	7680
tagatcaaaa	taatgcttta	actacgatata	acagaacttc	tcgcatttaat	gccaacttta	7740
gaatgtcaatt	ggggcagtgc	gcatacattt	atgcagaatg	tactgtatgt	gttgcggccgg	7800
cgggtgcagg	ttcattttgtct	tcccaagaata	atgaagacgt	ccgtgcggcc	tttctatgt	7860
atattgtatag	aactgtatgt	gggactttta	ttaataatgg	gaaacaacgt	tatgttcaag	7920
gcaatggctg	ctattcattta	tctacaggtc	cacagactgc	taattttccga	gttcatcattacc	7980
atggcggccg	agataacggt	tgatgttqaa	tgatgttqaa	tgggaaatttta	tgatgttqaa	8040

ttaaaaacgg tgattttatt tcacctcgcg atttaatagc aggcaaagtc agatttgata 8100
 gaactggtaa tatactggt gttctggta attttctaa cttaaacagt acaattgaat 8160
 cacttaaaac tgatatcatg tcgagttacc caattgggtgc tccgattccct tggccgagtg 8220
 attcagttcc tgctggattt gcttgcattt aaggttcagac ctttgataag tccgcataatc 8280
 caaagtttagc tggcataat cctagcggtg ttattccaga tatgcgcggg caaactatca 8340
 agggtaaacc aagtggtcgt gctgtttga gcgctgaggc agatggtgtt aaggctcata 8400
 gccatagttgc atcggcttca agtactgact taggtactaa aaccacatca agcttgcact 8460
 atggtagcggaa gggactaatac agtacgggtg gacacactca ctctggtagt ggttctacta 8520
 gcacaaatgg tgacacagc cactacatcg aggcatggaa tggtagtggt gtaggtggta 8580
 ataagatgtc atcatatgcc atatcataca gggcggtgg gagtaaact aatgcacgag 8640
 ggaaccacag tcacacttc tctttggga ctagcagtgc tggcgaccat tcccactctg 8700
 taggtattgg tgctcataacc cacacggtag caattggatc acatggtcat actatcactg 8760
 taaatagtagc aggtataatac gaaaacacgg taaaaacat tgcttttaac tatatcggtc 8820
 gtttagcata aggagagggg cttcgccct tctaa 8855

<210> 4
 <211> 1289
 <212> PRT
 <213> Bacteriophage T4

<400> 4
 Met Ala Glu Ile Lys Arg Glu Phe Arg Ala Glu Asp Gly Leu Asp Ala
 1 5 10 15
 Gly Gly Asp Lys Ile Ile Asn Val Ala Leu Ala Asp Arg Thr Val Gly
 20 25 30
 Thr Asp Gly Val Asn Val Asp Tyr Leu Ile Gln Glu Asn Thr Val Gln
 35 40 45
 Gln Tyr Asp Pro Thr Arg Gly Tyr Leu Lys Asp Phe Val Ile Ile Tyr
 50 55 60
 Asp Asn Arg Phe Trp Ala Ala Ile Asn Asp Ile Pro Lys Pro Ala Gly
 65 70 75 80
 Ala Phe Asn Ser Gly Arg Trp Arg Ala Leu Arg Thr Asp Ala Asn Trp
 85 90 95
 Ile Thr Val Ser Ser Gly Ser Tyr Gln Leu Lys Ser Gly Glu Ala Ile
 100 105 110
 Ser Val Asn Thr Ala Ala Gly Asn Asp Ile Thr Phe Thr Leu Pro Ser
 115 120 125
 Ser Pro Ile Asp Gly Asp Thr Ile Val Leu Gln Asp Ile Gly Gly Lys
 130 135 140
 Pro Gly Val Asn Gln Val Leu Ile Val Ala Pro Val Gln Ser Ile Val
 145 150 155 160
 Asn Phe Arg Gly Glu Gln Val Arg Ser Val Leu Met Thr His Pro Lys
 165 170 175
 Ser Gln Leu Val Leu Ile Phe Ser Asn Arg Leu Trp Gln Met Tyr Val
 180 185 190
 Ala Asp Tyr Ser Arg Glu Ala Ile Val Val Thr Pro Ala Asn Thr Tyr
 195 200 205
 Gln Ala Gln Ser Asn Asp Phe Ile Val Arg Arg Phe Thr Ser Ala Ala
 210 215 220
 Pro Ile Asn Val Lys Leu Pro Arg Phe Ala Asn His Gly Asp Ile Ile
 225 230 235 240

Asn Phe Val Asp Leu Asp Lys Leu Asn Pro Leu Tyr His Thr Ile Val
245 250 255

Thr Thr Tyr Asp Glu Thr Thr Ser Val Gln Glu Val Gly Thr His Ser
260 265 270

Ile Glu Gly Arg Thr Ser Ile Asp Gly Phe Leu Met Phe Asp Asp Asn
275 280 285

Glu Lys Leu Trp Arg Leu Phe Asp Gly Asp Ser Lys Ala Arg Leu Arg
290 295 300

Ile Ile Thr Thr Asn Ser Asn Ile Arg Pro Asn Glu Glu Val Met Val
305 310 315 320

Phe Gly Ala Asn Asn Gly Thr Thr Gln Thr Ile Glu Leu Lys Leu Pro
325 330 335

Thr Asn Ile Ser Val Gly Asp Thr Val Lys Ile Ser Met Asn Tyr Met
340 345 350

Arg Lys Gly Gln Thr Val Lys Ile Lys Ala Ala Asp Glu Asp Lys Ile
355 360 365

Ala Ser Ser Val Gln Leu Leu Gln Phe Pro Lys Arg Ser Glu Tyr Pro
370 375 380

Pro Glu Ala Glu Trp Val Thr Val Gln Glu Leu Val Phe Asn Asp Glu
385 390 395 400

Thr Asn Tyr Val Pro Val Leu Glu Leu Ala Tyr Ile Glu Asp Ser Asp
405 410 415

Gly Lys Tyr Trp Val Val Gln Gln Asn Val Pro Thr Val Glu Arg Val
420 425 430

Asp Ser Leu Asn Asp Ser Thr Arg Ala Arg Leu Gly Val Ile Ala Leu
435 440 445

Ala Thr Gln Ala Gln Ala Asn Val Asp Leu Glu Asn Ser Pro Gln Lys
450 455 460

Glu Leu Ala Ile Thr Pro Glu Thr Leu Ala Asn Arg Thr Ala Thr Glu
465 470 475 480

Thr Arg Arg Gly Ile Ala Arg Ile Ala Thr Thr Ala Gln Val Asn Gln
485 490 495

Asn Thr Thr Phe Ser Phe Ala Asp Asp Ile Ile Ile Thr Pro Lys Lys
500 505 510

Leu Asn Glu Arg Thr Ala Thr Glu Thr Arg Arg Gly Val Ala Glu Ile
515 520 525

Ala Thr Gln Gln Glu Thr Asn Ala Gly Thr Asp Asp Thr Thr Ile Ile
530 535 540

Thr Pro Lys Lys Leu Gln Ala Arg Gln Gly Ser Glu Ser Leu Ser Gly
545 550 555 560

Ile Val Thr Phe Val Ser Thr Ala Gly Ala Thr Pro Ala Ser Ser Arg
565 570 575

Glu Leu Asn Gly Thr Asn Val Tyr Asn Lys Asn Thr Asp Asn Leu Val

580	585	590
val Ser Pro Lys Ala Leu Asp Gln	Tyr Lys Ala Thr Pro Thr Gln Gln	
595 600	605	
Gly Ala Val Ile Leu Ala Val Glu Ser Glu Val Ile Ala Gly Gln Ser		
610 615	620	
Gln Gln Gly Trp Ala Asn Ala Val Val Thr Pro Glu Thr Leu His Lys		
625 630	635	640
Lys Thr Ser Thr Asp Gly Arg Ile Gly Leu Ile Glu Ile Ala Thr Gln		
645 650	655	
Ser Glu Val Asn Thr Gly Thr Asp Tyr Thr Arg Ala Val Thr Pro Lys		
660 665	670	
Thr Leu Asn Asp Arg Arg Ala Thr Glu Ser Leu Ser Gly Ile Ala Glu		
675 680	685	
Ile Ala Thr Gln Val Glu Phe Asp Ala Gly Val Asp Asp Thr Arg Ile		
690 695	700	
Ser Thr Pro Leu Lys Ile Lys Thr Arg Phe Asn Ser Thr Asp Arg Thr		
705 710	715	720
Ser Val Val Ala Leu Ser Gly Leu Val Glu Ser Gly Thr Leu Trp Asp		
725 730	735	
His Tyr Thr Leu Asn Ile Leu Glu Ala Asn Glu Thr Gln Arg Gly Thr		
740 745	750	
Leu Arg Val Ala Thr Gln Val Glu Ala Ala Ala Gly Thr Leu Asp Asn		
755 760	765	
Val Leu Ile Thr Pro Lys Lys Leu Leu Gly Thr Lys Ser Thr Glu Ala		
770 775	780	
Gln Glu Gly Val Ile Lys Val Ala Thr Gln Ser Glu Thr Val Thr Gly		
785 790	795	800
Thr Ser Ala Asn Thr Ala Val Ser Pro Lys Asn Leu Lys Trp Ile Ala		
805 810	815	
Gln Ser Glu Pro Thr Trp Ala Ala Thr Thr Ala Ile Arg Gly Phe Val		
820 825	830	
Lys Thr Ser Ser Gly Ser Ile Thr Phe Val Gly Asn Asp Thr Val Gly		
835 840	845	
Ser Thr Gln Asp Leu Glu Leu Tyr Glu Lys Asn Ser Tyr Ala Val Ser		
850 855	860	
Pro Tyr Glu Leu Asn Arg Val Leu Ala Asn Tyr Leu Pro Leu Lys Ala		
865 870	875	880
Lys Ala Ala Asp Thr Asn Leu Leu Asp Gly Leu Asp Ser Ser Gln Phe		
885 890	895	
Ile Arg Arg Asp Ile Ala Gln Thr Val Asn Gly Ser Leu Thr Leu Thr		
900 905	910	
Gln Gln Thr Asn Leu Ser Ala Pro Leu Val Ser Ser Ser Thr Gly Glu		
915 920	925	

Phe Gly Gly Ser Leu Ala Ala Asn Arg Thr Phe Thr Ile Arg Asn Thr
930 935 940

Gly Ala Pro Thr Ser Ile Val Phe Glu Lys Gly Pro Ala Ser Gly Ala
945 950 955 960

Asn Pro Ala Gln Ser Met Ser Ile Arg Val Trp Gly Asn Gln Phe Gly
965 970 975

Gly Gly Ser Asp Thr Thr Arg Ser Thr Val Phe Glu Val Gly Asp Asp
980 985 990

Thr Ser His His Phe Tyr Ser Gln Arg Asn Lys Asp Gly Asn Ile Ala
995 1000 1005

Phe Asn Ile Asn Gly Thr Val Met Pro Ile Asn Ile Asn Ala Ser Gly
1010 1015 1020

Leu Met Asn Val Asn Gly Thr Ala Thr Phe Gly Arg Ser Val Thr Ala
1025 1030 1035 1040

Asn Gly Glu Phe Ile Ser Lys Ser Ala Asn Ala Phe Arg Ala Ile Asn
1045 1050 1055

Gly Asp Tyr Gly Phe Phe Ile Arg Asn Asp Ala Ser Asn Thr Tyr Phe
1060 1065 1070

Leu Leu Thr Ala Ala Gly Asp Gln Thr Gly Gly Phe Asn Gly Leu Arg
1075 1080 1085

Pro Leu Leu Ile Asn Asn Gln Ser Gly Gln Ile Thr Ile Gly Glu Gly
1090 1095 1100

Leu Ile Ile Ala Lys Gly Val Thr Ile Asn Ser Gly Gly Leu Thr Val
1105 1110 1115 1120

Asn Ser Arg Ile Arg Ser Gln Gly Thr Lys Thr Ser Asp Leu Tyr Thr
1125 1130 1135

Arg Ala Pro Thr Ser Asp Thr Val Gly Phe Trp Ser Ile Asp Ile Asn
1140 1145 1150

Asp Ser Ala Thr Tyr Asn Gln Phe Pro Gly Tyr Phe Lys Met Val Glu
1155 1160 1165

Lys Thr Asn Glu Val Thr Gly Leu Pro Tyr Leu Glu Arg Gly Glu Glu
1170 1175 1180

Val Lys Ser Pro Gly Thr Leu Thr Gln Phe Gly Asn Thr Leu Asp Ser
1185 1190 1195 1200

Leu Tyr Gln Asp Trp Ile Thr Tyr Pro Thr Thr Pro Glu Ala Arg Thr
1205 1210 1215

Thr Arg Trp Thr Arg Thr Trp Gln Lys Thr Lys Asn Ser Trp Ser Ser
1220 1225 1230

Phe Val Gln Val Phe Asp Gly Gly Asn Pro Pro Gln Pro Ser Asp Ile
1235 1240 1245

Gly Ala Leu Pro Ser Asp Asn Ala Thr Met Gly Asn Leu Thr Ile Arg
1250 1255 1260

Asp Phe Leu Arg Ile Gly Asn Val Arg Ile Val Pro Asp Pro Val Asn
1265 1270 1275 1280

Lys Thr Val Lys Phe Glu Trp Val Glu
1285

<210> 5
<211> 65
<212> PRT
<213> Bacteriophage T4

<400> 5
Met Glu Lys Phe Met Ala Glu Ile Trp Thr Arg Ile Cys Pro Asn Ala
1 5 10 15

Ile Leu Ser Glu Ser Asn Ser Val Arg Tyr Lys Ile Ser Ile Ala Gly
20 25 30

Ser Cys Pro Leu Ser Thr Ala Gly Pro Ser Tyr Val Lys Phe Gln Asp
35 40 45

Asn Pro Val Gly Ser Gln Thr Phe Arg Arg Arg Pro Ser Phe Lys Ser
50 55 60

Phe
65

<210> 6
<211> 295
<212> PRT
<213> Bacteriophage T4

<400> 6
Met Leu Phe Arg Leu Gln Met Ile Leu His Gln Leu Leu Leu Leu Val
1 5 10 15

Phe Met Asn Ser Leu Thr Asn Asn Arg Ile Val Ala Ile Leu Thr Ser
20 25 30

Gly Lys Val Asn Phe Pro Pro Glu Val Val Ser Trp Leu Arg Thr Ala
35 40 45

Gly Thr Ser Ala Phe Pro Ser Asp Ser Ile Leu Ser Arg Phe Asp Val
50 55 60

Ser Tyr Ala Ala Phe Tyr Thr Ser Ser Lys Arg Ala Ile Ala Leu Glu
65 70 75 80

His Val Lys Leu Ser Asn Arg Lys Ser Thr Asp Asp Tyr Gln Thr Ile
85 90 95

Leu Asp Val Val Phe Asp Ser Leu Glu Asp Val Gly Ala Thr Gly Phe
100 105 110

Pro Arg Arg Thr Tyr Glu Ser Val Glu Gln Phe Met Ser Ala Val Gly
115 120 125

Gly Thr Asn Asn Glu Ile Ala Arg Leu Pro Thr Ser Ala Ala Ile Ser
130 135 140

Lys Leu Ser Asp Tyr Asn Leu Ile Pro Gly Asp Val Leu Tyr Leu Lys
145 150 155 160

Ala Gln Leu Tyr Ala Asp Ala Asp Leu Leu Ala Leu Gly Thr Thr Asn
165 170 175

Ile Ser Ile Arg Phe Tyr Asn Ala Ser Asn Gly Tyr Ile Ser Ser Thr
180 185 190
Gln Ala Glu Phe Thr Gly Gln Ala Gly Ser Trp Glu Leu Lys Glu Asp
195 200 205
Tyr Val Val Val Pro Glu Asn Ala Val Gly Phe Thr Ile Tyr Ala Gln
210 215 220
Arg Thr Ala Gln Ala Gly Gln Gly Gly Met Arg Asn Leu Ser Phe Ser
225 230 235 240
Glu Val Ser Arg Asn Gly Gly Ile Ser Lys Pro Ala Glu Phe Gly Val
245 250 255
Asn Gly Ile Arg Val Asn Tyr Ile Cys Glu Ser Ala Ser Pro Pro Asp
260 265 270
Ile Met Val Leu Pro Thr Gln Ala Ser Ser Lys Thr Gly Lys Val Phe
275 280 285
Gly Gln Glu Phe Arg Glu Val
290 295

<210> 7
<211> 221
<212> PRT
<213> Bacteriophage T4

<400> 7
Met Ala Asp Leu Lys Val Gly Ser Thr Thr Gly Gly Ser Val Ile Trp
1 5 10 15
His Gln Gly Asn Phe Pro Leu Asn Pro Ala Gly Asp Asp Val Leu Tyr
20 25 30
Lys Ser Phe Lys Ile Tyr Ser Glu Tyr Asn Lys Pro Gln Ala Ala Asp
35 40 45
Asn Asp Phe Val Ser Lys Ala Asn Gly Gly Thr Tyr Ala Ser Lys Val
50 55 60
Thr Phe Asn Ala Gly Ile Gln Val Pro Tyr Ala Pro Asn Ile Met Ser
65 70 75 80
Pro Cys Gly Ile Tyr Gly Gly Asn Gly Asp Gly Ala Thr Phe Asp Lys
85 90 95
Ala Asn Ile Asp Ile Val Ser Trp Tyr Gly Val Gly Phe Lys Ser Ser
100 105 110
Phe Gly Ser Thr Gly Arg Thr Val Val Ile Asn Thr Arg Asn Gly Asp
115 120 125
Ile Asn Thr Lys Gly Val Val Ser Ala Ala Gly Gln Val Arg Ser Gly
130 135 140
Ala Ala Ala Pro Ile Ala Ala Asn Asp Leu Thr Arg Lys Asp Tyr Val
145 150 155 160
Asp Gly Ala Ile Asn Thr Val Thr Ala Asn Ala Asn Ser Arg Val Leu
165 170 175

Arg Ser Gly Asp Thr Met Thr Gly Asn Leu Thr Ala Pro Asn Phe Phe
180 185 190

Ser Gln Asn Pro Ala Ser Gln Pro Ser His Val Pro Arg Phe Asp Gln
195 200 205

Ile Val Ile Lys Asp Ser Val Gln Asp Phe Gly Tyr Tyr
210 215 220

<210> 8

<211> 1026

<212> PRT

<213> Bacteriophage T4

<400> 8

Met Ala Thr Leu Lys Gln Ile Gln Phe Lys Arg Ser Lys Ile Ala Gly
1 5 10 15

Thr Arg Pro Ala Ala Ser Val Leu Ala Glu Gly Glu Leu Ala Ile Asn
20 25 30

Leu Lys Asp Arg Thr Ile Phe Thr Lys Asp Asp Ser Gly Asn Ile Ile
35 40 45

Asp Leu Gly Phe Ala Lys Gly Gln Val Asp Gly Asn Val Thr Ile
50 55 60

Asn Gly Leu Leu Arg Leu Asn Gly Asp Tyr Val Gln Thr Gly Gly Met
65 70 75 80

Thr Val Asn Gly Pro Ile Gly Ser Thr Asp Gly Val Thr Gly Lys Ile
85 90 95

Phe Arg Ser Thr Gln Gly Ser Phe Tyr Ala Arg Ala Thr Asn Asp Thr
100 105 110

Ser Asn Ala His Leu Trp Phe Glu Asn Ala Asp Gly Thr Glu Arg Gly
115 120 125

Val Ile Tyr Ala Arg Pro Gln Thr Thr Asp Gly Glu Ile Arg Leu
130 135 140

Arg Val Arg Gln Gly Thr Gly Ser Thr Ala Asn Ser Glu Phe Tyr Phe
145 150 155 160

Arg Ser Ile Asn Gly Gly Glu Phe Gln Ala Asn Arg Ile Leu Ala Ser
165 170 175

Asp Ser Leu Val Thr Lys Arg Ile Ala Val Asp Thr Val Ile His Asp
180 185 190

Ala Lys Ala Phe Gly Gln Tyr Asp Ser His Ser Leu Val Asn Tyr Val
195 200 205

Tyr Pro Gly Thr Gly Glu Thr Asn Gly Val Asn Tyr Leu Arg Lys Val
210 215 220

Arg Ala Lys Ser Gly Gly Thr Ile Tyr His Glu Ile Val Thr Ala Gln
225 230 235 240

Thr Gly Leu Ala Asp Glu Val Ser Trp Trp Ser Gly Asp Thr Pro Val
245 250 255

Phe Lys Leu Tyr Gly Ile Arg Asp Asp Gly Arg Met Ile Ile Arg Asn

260

265

270

Ser Leu Ala Leu Gly Thr Phe Thr Thr Asn Phe Pro Ser Ser Asp Tyr
275 280 285

Gly Asn Val Gly Val Met Gly Asp Lys Tyr Leu Val Leu Gly Asp Thr
290 295 300

Val Thr Gly Leu Ser Tyr Lys Lys Thr Gly Val Phe Asp Leu Val Gly
305 310 315 320

Gly Gly Tyr Ser Val Ala Ser Ile Thr Pro Asp Ser Phe Arg Ser Thr
325 330 335

Arg Lys Gly Ile Phe Gly Arg Ser Glu Asp Gln Gly Ala Thr Trp Ile
340 345 350

Met Pro Gly Thr Asn Ala Ala Leu Leu Ser Val Gln Thr Gln Ala Asp
355 360 365

Asn Asn Asn Ala Gly Asp Gly Gln Thr His Ile Gly Tyr Asn Ala Gly
370 375 380

Gly Lys Met Asn His Tyr Phe Arg Gly Thr Gly Gln Met Asn Ile Asn
385 390 395 400

Thr Gln Gln Gly Met Glu Ile Asn Pro Gly Ile Leu Lys Leu Val Thr
405 410 415

Gly Ser Asn Asn Val Gln Phe Tyr Ala Asp Gly Thr Ile Ser Ser Ile
420 425 430

Gln Pro Ile Lys Leu Asp Asn Glu Ile Phe Leu Thr Lys Ser Asn Asn
435 440 445

Thr Ala Gly Leu Lys Phe Gly Ala Pro Ser Gln Val Asp Gly Thr Arg
450 455 460

Thr Ile Gln Trp Asn Gly Gly Thr Arg Glu Gly Gln Asn Lys Asn Tyr
465 470 475 480

Val Ile Ile Lys Ala Trp Gly Asn Ser Phe Asn Ala Thr Gly Asp Arg
485 490 495

Ser Arg Glu Thr Val Phe Gln Val Ser Asp Ser Gln Gly Tyr Tyr Phe
500 505 510

Tyr Ala His Arg Lys Ala Pro Thr Gly Asp Glu Thr Ile Gly Arg Ile
515 520 525

Glu Ala Gln Phe Ala Gly Asp Val Tyr Ala Lys Gly Ile Ile Ala Asn
530 535 540

Gly Asn Phe Arg Val Val Gly Ser Ser Ala Leu Ala Gly Asn Val Thr
545 550 555 560

Met Ser Asn Gly Leu Phe Val Gln Gly Gly Ser Ser Ile Thr Gly Gln
565 570 575

Val Lys Ile Gly Gly Thr Ala Asn Ala Leu Arg Ile Trp Asn Ala Glu
580 585 590

Tyr Gly Ala Ile Phe Arg Arg Ser Glu Ser Asn Phe Tyr Ile Ile Pro
595 600 605

Thr Asn Gln Asn Glu Gly Glu Ser Gly Asp Ile His Ser Ser Leu Arg
610 615 620

Pro Val Arg Ile Gly Leu Asn Asp Gly Met Val Gly Leu Gly Arg Asp
625 630 635 640

Ser Phe Ile Val Asp Gln Asn Asn Ala Leu Thr Thr Ile Asn Ser Asn
645 650 655

Ser Arg Ile Asn Ala Asn Phe Arg Met Gln Leu Gly Gln Ser Ala Tyr
660 665 670

Ile Asp Ala Glu/Cys Thr Asp Ala Val Arg Pro Ala Gly Ala Gly Ser
675 680 685

Phe Ala Ser Gln Asn Asn Glu Asp Val Arg Ala Pro Phe Tyr Met Asn
690 695 700

Ile Asp Arg Thr Asp Ala Ser Ala Tyr Val Pro Ile Leu Lys Gln Arg
705 710 715 720

Tyr Val Gln Gly Asn Gly Cys Tyr Ser Leu Gly Thr Leu Ile Asn Asn
725 730 735

Gly Asn Phe Arg Val His Tyr His Gly Gly Asp Asn Gly Ser Thr
740 745 750

Gly Pro Gln Thr Ala Asp Phe Gly Trp Glu Phe Ile Lys Asn Gly Asp
755 760 765

Phe Ile Ser Pro Arg Asp Leu Ile Ala Gly Lys Val Arg Phe Asp Arg
770 775 780

Thr Gly Asn Ile Thr Gly Gly Ser Gly Asn Phe Ala Asn Leu Asn Ser
785 790 795 800

Thr Ile Glu Ser Leu Lys Thr Asp Ile Met Ser Ser Tyr Pro Ile Gly
805 810 815

Ala Pro Ile Pro Trp Pro Ser Asp Ser Val Pro Ala Gly Phe Ala Leu
820 825 830

Met Glu Gly Gln Thr Phe Asp Lys Ser Ala Tyr Pro Lys Leu Ala Val
835 840 845

Ala Tyr Pro Ser Gly Val Ile Pro Asp Met Arg Gly Gln Thr Ile Lys
850 855 860

Gly Lys Pro Ser Gly Arg Ala Val Leu Ser Ala Glu Ala Asp Gly Val
865 870 875 880

Lys Ala His Ser His Ser Ala Ser Ala Ser Ser Thr Asp Leu Gly Thr
885 890 895

Lys Thr Thr Ser Ser Phe Asp Tyr Gly Thr Lys Gly Thr Asn Ser Thr
900 905 910

Gly Gly His Thr His Ser Gly Ser Gly Ser Thr Ser Thr Asn Gly Glu
915 920 925

His Ser His Tyr Ile Glu Ala Trp Asn Gly Thr Gly Val Gly Gly Asn
930 935 940

Lys Met Ser Ser Tyr Ala Ile Ser Tyr Arg Ala Gly Gly Ser Asn Thr
945 950 955 960

Asn Ala Ala Gly Asn His Ser His Thr Phe Ser Phe Gly Thr Ser Ser
965 970 975

Ala Gly Asp His Ser His Ser Val Gly Ile Gly Ala His Thr His Thr
980 985 990

Val Ala Ile Gly Ser His Gly His Thr Ile Thr Val Asn Ser Thr Gly
995 1000 1005

Asn Thr Glu Asn Thr Val Lys Asn Ile Ala Phe Asn Tyr Ile Val Arg
1010 1015 1020

Leu Ala
1025